



	TCATTTTTCAT	CATCATCGTA	AATGGTTACG	CAAAAGATAT	TTCTGGAGTT	AAAAGAGGTC	840
	ATGAACGACT	TAACGAATAC	ATATCCCCT	ATGAAACACT	CAACTATGAT	CACGAGCACA	900
	TCCGAGCTAG	TCACAATAGA	GCGCGACGAT	CAGTGACCAA	AGATCAATAT	GTACATTTAA	960
	AGTTTGCATC	ACATGGAAGA	GACTTCCATC	TTAGATTAAA	ACGTGATTTA	AATACATTTA	1020
5	GCAATAAGTT	AGACTTTTAT	GATAGCAAAG	GTCCCATTTGA	TGTCTCCACG	GATCATATCT	1080
	ATGAGGGCGA	AGTGATAGGG	GATCGTAATA	GTTATGTATT	TGGTTCCATA	CACAATGGGG	1140
	TATTCGAGGG	TAAAATTATA	ACGGAACGTG	ATGCCTATTA	TGTTGAACAT	GCCAAACATT	1200
	ATTTTCCCAC	AAATCGCACG	GCGACAACAA	CACCACCATC	GACTTCGACG	ACATCCTCAG	1260
	CAACAACAGT	CACAAAAAGC	ACACAACCAA	CACGGCCTTT	GGCCAAAAGC	AACACCAGTA	1320
10	CTACTGCCGT	TAATAGTAAG	ACAGAAAAC	TTATAAAGAA	AATTGCTGAA	TCCACAACGA	1380
	CGAGCCAGCA	GCTTCCAGAA	TATACCGAAT	CGTCGTCGTC	GTCGTCGACA	ACAACATTCC	1440
	CACCCACAAC	AGAGTATTTT	GAGGACGAAA	AGGAGCGTAA	TGCCGAGGAC	GAAGTTGATT	1500
	TTCACTCCAT	TATCTACAAG	GAGTCACATG	TCGAGGACGC	CTACGAAAAT	GTGCGCGAAG	1560
	GTCACGTGGC	CGGCTGTGGC	ATCACGGATG	AGGTCTCTCA	GTGGATGGAG	AACATACAAA	1620
15	ATTCAGCCGT	CGAAGAGTTG	CCGGAGCCCA	TGTCAAAGGA	CTATCAAAG	CTCCACCGGA	1680
	AGCAGCTGCA	CAAAAAGTCC	GCCCCACAGC	AACAACAGCA	GCCCCATCCG	CCGAAGAAGT	1740
	ACATCAGCGG	GGATGAGGAC	TTCAAGTATC	CCCACCAGAA	GTACACGAAG	GAAGCTAACT	1800
	TCGCCGAGGG	TGCATTCTAC	GATCCATCGA	CCGGACGTCG	CCTGGGCTCA	TCCGCCAACG	1860
	TGGCCGACTG	GCATCAGCTC	GTCCACGAGC	GCGTCCGCCG	CGCCACCGAC	AATGGTGCTG	1920
20	GGGATAGGGG	CTCATCCGGT	GGATCTGGAC	GCGGTCGCGA	GGACAACAAG	AATACCTGCT	1980
	CGCTCTACAT	TCAAACGGAT	CCATTGATAT	GGCGCCACAT	ACGCGAAGGC	ATTGCTGACC	2040
	ACGATCGTGG	ACGCAAGTAC	GAGGTGGATG	AGAAAACGCG	CGAGGAAATC	ACATCGTTGA	2100
	TTGCACATCA	CGTGACGGCC	GTTAATTACA	TTTACCGCAA	CACAAAGTTC	GACGGACGCA	2160
	CCGAGCATCG	CAACATACGC	TTTGAGGTGC	AACGCATTAA	GATCGATGAC	GATTCGGCCT	2220
25	GTCGCAATTC	CTACAATGGT	CCACACAATG	CCTTTTGCAA	TGAACACATG	GATGTCTCGA	2280
	ACTTTTTTGAA	TCTGCATTCC	CTAGAAGATC	ACTCGGACTT	TTGTTTGGCT	TACGTGTTCA	2340
	CCTACAGAGA	TTTCACTGGC	GGCACTTTGG	GTCTGGCCTG	GGTGGCCAGT	GCGTCGGGAG	2400
	CCTCTGGTGG	AATTTGCGAG	AAGTACAAGA	CGTACACGGA	AACGGTGGGT	GGACAGTACC	2460
	AGAGCACCAA	GCGATCACTC	AACACGGGCA	TCATCACCTT	TGTCAACTAC	AACAGTCGGG	2520
30	TGCCGCCGAA	AGTGTGCGAG	CTTACGTTGG	CACACGAGAT	TGGCCACAAC	TTTGGATCAC	2580
	CTCACGATTA	CCCTCAGGAA	TGTCGTCCTG	GTGGCCTAAA	TGGCAATTAC	ATTATGTTTC	2640
	CCAGTGCCAC	CTCCGGTGAT	AGGCCAAATA	ACTCCAAGTT	CTCGCCCTGC	TCCATTCGGA	2700
	ACATCTCCAA	TGTCCTTGAC	GTGCTGGTGG	GCAACACGAA	GCGCGACTGC	TTCAAGGCCT	2760
	CGGAAGGTGC	CTTCTGCGGC	AACAAGATCG	TGGAGTCTGG	CGAGGAATGC	GACTGTGGCT	2820
35	TCAACGAGGA	GGAGTGCAAG	GACAAGTGCT	GCTACCCGCG	TCTGATCAGC	GAGTACGACC	2880
	AGTCGCTGAA	CTCCAGTGCC	AAGGGATGCA	CGCGCCGCGC	CAAGACCCAG	TGCTCACCAT	2940
	CGCAGGGTCC	GTGCTGTCTG	TCCAACCTCT	GCACCTTTGT	GCCGACGAGC	TACCACCAGA	3000
	AGTGCAAGGA	GGAGACGGAG	TGCAGCTGGT	CGAGCACATG	CAACGGAACC	ACGGCCGAGT	3060
	GTCCGGAGCC	ACGTCATCGC	GATGACAAGA	CCATGTGCAA	CAATGGAACA	GCGCTATGCA	3120
40	TCCGCGGTGA	ATGTAGTGGA	TCGCCATGTT	TGCTCTGGAA	TATGACAAAG	TGCTTCCTTA	3180
	CCTCGACCAC	ACTGCCGCAC	GTGAGCAAGC	GCAAGTTGTG	CGACTTGGCC	TGCCAGGATG	3240
	GCAATGACAC	CTCCACCTGC	CGCAGCACCA	GCGAGTTTGC	CGATAAATAT	AATATTCAAA	3300
	AGGGTGGTAT	TAGTCTGCAG	CCCGGTTTCG	CATGCGATAA	TTTCCAGGGC	TACTGCGATG	3360
	TGTTCCCTTAA	GTGTCGAGCC	GTGGATGCCG	ATGGTCCGCT	TCTTCGGCTG	AAGAATTTGT	3420
45	TGCTCAACCG	GAAGACCCTG	CAAACGGTGG	CCGAGTGGAT	CGTCGACAAT	TGGTACCTAG	3480
	TGGTTCTGAT	GGGAGTGGCC	TTTATTGTGG	TCATGGGTTC	GTTTCATCAA	TGTTGTGCCG	3540
	TGCACACGCC	CAGTTCCAAT	CCGAAGAAGC	GACGAGCTCG	TCGAATCAGC	GAAACTCTAA	3600
	GAGCACCCAT	GAACACGTTG	CGTAGAATGC	AACGTCATCC	CAATCAGCGA	GGAGCAGGTC	3660
	CTCGAAGCAT	CCCACCGCCG	GCACATGAGG	CGCAGCATTA	TTCACGCGGC	GGAGATGGTC	3720
50	GCGGCGGCGG	CGGTGGAGGC	GGAGGTCGCC	ACGGTGGCTC	TAGGTACACAC	CATCAACAGC	3780
	ATCCGCACGA	TTGGGATCGT	CATCAGGGTG	GCCACTCAAT	CGTCCCATTG	CCCACCGGCG	3840
	GCAGCCATTG	AAGTCGCAAC	TCGGCGGCGA	ATCAAGCGAG	AAGAAGCGAT	GGACGAGGTC	3900
	CACGATCCAC	CAGCAGTGGG	CGGCCGCAGG	CTATAGCCAG	CGGAAGCGGT	GCCGCGAGCG	3960
	GAGCAGCGCG	ATCTCATGGC	GGGTACGGAG	CCGAACAGGC	GATACCGGGT	TCCATTGGTG	4020
55	GTGGTGTCCA	GGCGGCCATT	AGCAGCGGCG	GTGTGGTGGC	TCGGGCCCAG	CTGCCGCTGC	4080

	CATTGCCGCC	GCCAAATGGA	CAGCAGCAAA	TGCAACAGCA	ACAACAACCTG	CAACTACAGC	4140
	AACCGGCAAT	TTCGCCGCAG	CAGCAGCCGC	AGCAAGCGTT	CTACACGCCG	AAAGAACTAC	4200
	CACCACGCAA	TAAGTCCCGA	TCATCACGTA	CCAACAACAC	CTCCAACACC	ACAACCACCA	4260
	CCAACTCATC	CACAGCGGCA	GCCGGCAGTG	GGTCGGTCTC	GGGACCGGGC	TCGGGGGCGG	4320
5	GCAGTAGTAG	TAAGAGCAAG	AGCGGTAAAA	GTGCCAAAGC	CAAAGACTCA	AAGTCGCAAA	4380
	AATCGCAGCA	GGCCAACAAC	AGTCGCAGCA	GCAGCAAGGA	GAAGGGCGTC	AAGCCAGTGC	4440
	GCCGAAATAT	CGTTTATTAG	GAGCGGAACC	ATCACATTGC	CATACACAAC	ACTGAACGAA	4500
	ATATAGCCCC	GAACCCAAAA	TATCAAATGC	AACCACATAT	AGAATCGCCC	GCTGCTAGTC	4560
	ATCGAACTAC	ATGTATGAGT	TGTTGCTTCC	CATCCACCGA	CAAACACAAA	CAGAAAAGAA	4620
10	ATTATAATGA	TATTTTCATTT	AATCGATGCA	ATTGGCGTCG	CGCCGCCTCC	GCTACAAGTA	4680
	AGCTTTAGTC	GGCCGACATC	GTTGCACGAG	CAACAGCAGC	AGCAACATCA	TCTGCAGCAG	4740
	CAGCAGCAGC	ATCAGCAGCA	ACTGGAGCCG	CAGCAGCAAC	ACGCCTATGC	CGATGCTTAT	4800
	GCGGCCTTGG	GGCGGGGCCA	GTATGAGTCC	ACCACGCGGG	CGCCCAACAA	CAGCAAGGTT	4860
	TGACAGCCAA	AAGTAGCAAT	GGAGCGCCAC	AAAAGGCCAA	AGGCTAAGCG	ACTCAAGCAG	4920
15	CAGAAGGAGC	CGCATACACA	GCAAACAACA	ACACAGCAAC	AAAAGCAAAA	ACAACATAAA	4980
	TCAAATGAAC	TCAAATTAAA	TGTAAATGTA	ATTTTTATGC	TAATTATTTT	TATTTAAACA	5040
	GTGTTTGTAT	GCCACAAGGG	AAACAGCCA	GCAACAAAAA	GAAAAATACA	AAAATAACAC	5100
	AAAAAAGGAG	ACAAATTTTCG	TAATACAGAA	AAAGCTGAAA	GTGAATGATA	TTTTTGATTA	5160
	ACTAAATTAA	AATGAAAATA	CGAATGCAAA	TTATGAATAA	TAAAAGTAAT	TAAAAACGAC	5220
20	AACATGCATA	ATACATATAA	AGTTGCAAGT	TGCATATATA	TACATTTGTA	TGTATATATT	5280
	TATTATGGAT	ACACAATTAT	TAAATAGCAG	CAGCCACAAC	AAACAAGTAA	TATACATGAA	5340
	GAAAAACTAA	GGTTTAATTG	TATGAGAAAG	CATTCTATAT	GTCGGTGAGA	TTTCTAAGCG	5400
	CTAGGCCGAA	ATACAAAATT	AATTACACAC	TTGAATAACA	AAATGTGTTT	TGTACAAAAA	5460
	AAAAAAAATG	AAATAAACAA	AAACAGTGCG	AATTAATTAA	GCGTCATTAT	AAAAAAAAGA	5520
25	ACGGAAACAA	CAAAGCATTT	AAATTGTATT	TATCTGTACC	GAAGCTAAAC	GTTTATTTAA	5580
	AGCCGTCAAA	ATTGCATTTG	TAAACTAGCA	AAACAAAAAA	AAAAAAAAC		5630

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1239 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Ser	Lys	Cys	Ala	Phe	Asn	Ile	Val	Phe	Val	Ser	Ile	Ile	Phe
1				5					10					15	
Ile	Ile	Ile	Val	Asn	Gly	Tyr	Ala	Lys	Asp	Ile	Ser	Gly	Val	Lys	Arg
			20					25					30		
Gly	His	Glu	Arg	Leu	Asn	Glu	Tyr	Ile	Ser	His	Tyr	Glu	Thr	Leu	Asn
			35				40					45			
Tyr	Asp	His	Glu	His	Ile	Arg	Ala	Ser	His	Asn	Arg	Ala	Arg	Arg	Ser
	50					55				60					
Val	Thr	Lys	Asp	Gln	Tyr	Val	His	Leu	Lys	Phe	Ala	Ser	His	Gly	Arg
65					70					75				80	
Asp	Phe	His	Leu	Arg	Leu	Lys	Arg	Asp	Leu	Asn	Thr	Phe	Ser	Asn	Lys
			85					90					95		
Leu	Asp	Phe	Tyr	Asp	Ser	Lys	Gly	Pro	Ile	Asp	Val	Ser	Thr	Asp	His
			100				105					110			
Ile	Tyr	Glu	Gly	Glu	Val	Ile	Gly	Asp	Arg	Asn	Ser	Tyr	Val	Phe	Gly
		115					120					125			
Ser	Ile	His	Asn	Gly	Val	Phe	Glu	Gly	Lys	Ile	Ile	Thr	Glu	Arg	Asp
		130				135						140			
Ala	Tyr	Tyr	Val	Glu	His	Ala	Lys	His	Tyr	Phe	Pro	Thr	Asn	Arg	Thr
145					150					155					160

	Ala	Thr	Thr	Thr	Pro	Pro	Ser	Thr	Ser	Thr	Thr	Ser	Ser	Ala	Thr	Thr	
					165					170					175		
	Val	Thr	Lys	Ser	Thr	Gln	Pro	Thr	Arg	Pro	Leu	Ala	Lys	Ser	Asn	Thr	
				180					185					190			
5	Ser	Thr	Thr	Ala	Val	Asn	Ser	Lys	Thr	Glu	Asn	Phe	Ile	Lys	Lys	Ile	
			195					200				205					
	Ala	Glu	Ser	Thr	Thr	Thr	Ser	Gln	Gln	Leu	Pro	Glu	Tyr	Thr	Glu	Ser	
		210					215					220					
	Ser	Ser	Ser	Ser	Ser	Thr	Thr	Thr	Phe	Pro	Pro	Thr	Thr	Glu	Tyr	Phe	
10	225					230				235						240	
	Glu	Asp	Glu	Lys	Glu	Arg	Asn	Ala	Glu	Asp	Glu	Leu	Asp	Phe	His	Ser	
					245					250					255		
	Ile	Ile	Tyr	Lys	Glu	Ser	His	Val	Glu	Asp	Ala	Tyr	Glu	Asn	Val	Arg	
				260					265					270			
15	Glu	Gly	His	Val	Ala	Gly	Cys	Gly	Ile	Thr	Asp	Glu	Val	Ser	Gln	Trp	
			275					280					285				
	Met	Glu	Asn	Ile	Gln	Asn	Ser	Ala	Val	Glu	Glu	Leu	Pro	Glu	Pro	Met	
		290				295						300					
	Ser	Lys	Asp	Tyr	Gln	Lys	Leu	His	Arg	Lys	Gln	Leu	His	Lys	Lys	Ser	
20	305					310					315					320	
	Ala	Pro	Gln	Gln	Gln	Gln	Gln	Pro	His	Pro	Pro	Lys	Lys	Tyr	Ile	Ser	
					325					330					335		
	Gly	Asp	Glu	Asp	Phe	Lys	Tyr	Pro	His	Gln	Lys	Tyr	Thr	Lys	Glu	Ala	
				340				345						350			
25	Asn	Phe	Ala	Glu	Gly	Ala	Phe	Tyr	Asp	Pro	Ser	Thr	Gly	Arg	Arg	Leu	
		355					360						365				
	Gly	Ser	Ser	Ala	Asn	Val	Ala	Asp	Trp	His	Gln	Leu	Val	His	Glu	Arg	
		370				375						380					
	Val	Arg	Arg	Ala	Thr	Asp	Asn	Gly	Ala	Gly	Asp	Arg	Gly	Ser	Ser	Gly	
30	385					390					395					400	
	Gly	Ser	Gly	Arg	Gly	Arg	Glu	Asp	Asn	Lys	Asn	Thr	Cys	Ser	Leu	Tyr	
				405						410					415		
	Ile	Gln	Thr	Asp	Pro	Leu	Ile	Trp	Arg	His	Ile	Arg	Glu	Gly	Ile	Ala	
				420					425					430			
35	Asp	His	Asp	Arg	Gly	Arg	Lys	Tyr	Glu	Val	Asp	Glu	Lys	Thr	Arg	Glu	
		435					440						445				
	Glu	Ile	Thr	Ser	Leu	Ile	Ala	His	His	Val	Thr	Ala	Val	Asn	Tyr	Ile	
		450				455						460					
	Tyr	Arg	Asn	Thr	Lys	Phe	Asp	Gly	Arg	Thr	Glu	His	Arg	Asn	Ile	Arg	
40	465					470					475					480	
	Phe	Glu	Val	Gln	Arg	Ile	Lys	Ile	Asp	Asp	Asp	Ser	Ala	Cys	Arg	Asn	
				485					490					495			
	Ser	Tyr	Asn	Gly	Pro	His	Asn	Ala	Phe	Cys	Asn	Glu	His	Met	Asp	Val	
			500						505					510			
45	Ser	Asn	Phe	Leu	Asn	Leu	His	Ser	Leu	Glu	Asp	His	Ser	Asp	Phe	Cys	
		515					520						525				
	Leu	Ala	Tyr	Val	Phe	Thr	Tyr	Arg	Asp	Phe	Thr	Gly	Gly	Thr	Leu	Gly	
		530					535					540					
	Leu	Ala	Trp	Val	Ala	Ser	Ala	Ser	Gly	Ala	Ser	Gly	Gly	Ile	Cys	Glu	
50	545					550					555					560	
	Lys	Tyr	Lys	Thr	Tyr	Thr	Glu	Thr	Val	Gly	Gly	Gln	Tyr	Gln	Ser	Thr	
				565						570				575			
	Lys	Arg	Ser	Leu	Asn	Thr	Gly	Ile	Ile	Thr	Phe	Val	Asn	Tyr	Asn	Ser	
				580					585				590				
55	Arg	Val	Pro	Pro	Lys	Val	Ser	Gln	Leu	Thr	Leu	Ala	His	Glu	Ile	Gly	

		595				600				605							
		His	Asn	Phe	Gly	Ser	Pro	His	Asp	Tyr	Pro	Gln	Glu	Cys	Arg	Pro	Gly
		610						615				620					
5		Gly	Leu	Asn	Gly	Asn	Tyr	Ile	Met	Phe	Ala	Ser	Ala	Thr	Ser	Gly	Asp
		625					630					635				640	
		Arg	Pro	Asn	Asn	Ser	Lys	Phe	Ser	Pro	Cys	Ser	Ile	Arg	Asn	Ile	Ser
						645					650					655	
		Asn	Val	Leu	Asp	Val	Leu	Val	Gly	Asn	Thr	Lys	Arg	Asp	Cys	Phe	Lys
					660					665					670		
10		Ala	Ser	Glu	Gly	Ala	Phe	Cys	Gly	Asn	Lys	Ile	Val	Glu	Ser	Gly	Glu
					675				680					685			
		Glu	Cys	Asp	Cys	Gly	Phe	Asn	Glu	Glu	Glu	Cys	Lys	Asp	Lys	Cys	Cys
					690			695					700				
15		Tyr	Pro	Arg	Leu	Ile	Ser	Glu	Tyr	Asp	Gln	Ser	Leu	Asn	Ser	Ser	Ala
		705					710					715					720
		Lys	Gly	Cys	Thr	Arg	Arg	Ala	Lys	Thr	Gln	Cys	Ser	Pro	Ser	Gln	Gly
						725					730					735	
		Pro	Cys	Cys	Leu	Ser	Asn	Ser	Cys	Thr	Phe	Val	Pro	Thr	Ser	Tyr	His
					740					745					750		
20		Gln	Lys	Cys	Lys	Glu	Glu	Thr	Glu	Cys	Ser	Trp	Ser	Ser	Thr	Cys	Asn
					755				760						765		
		Gly	Thr	Thr	Ala	Glu	Cys	Pro	Glu	Pro	Arg	His	Arg	Asp	Asp	Lys	Thr
					770				775				780				
25		Met	Cys	Asn	Asn	Gly	Thr	Ala	Leu	Cys	Ile	Arg	Gly	Glu	Cys	Ser	Gly
		785					790					795					800
		Ser	Pro	Cys	Leu	Leu	Trp	Asn	Met	Thr	Lys	Cys	Phe	Leu	Thr	Ser	Thr
						805					810					815	
		Thr	Leu	Pro	His	Val	Ser	Lys	Arg	Lys	Leu	Cys	Asp	Leu	Ala	Cys	Gln
					820					825					830		
30		Asp	Gly	Asn	Asp	Thr	Ser	Thr	Cys	Arg	Ser	Thr	Ser	Glu	Phe	Ala	Asp
					835				840					845			
		Lys	Tyr	Asn	Ile	Gln	Lys	Gly	Gly	Ile	Ser	Leu	Gln	Pro	Gly	Ser	Pro
					850			855					860				
		Cys	Asp	Asn	Phe	Gln	Gly	Tyr	Cys	Asp	Val	Phe	Leu	Lys	Cys	Arg	Ala
35		865					870					875					880
		Val	Asp	Ala	Asp	Gly	Pro	Leu	Leu	Arg	Leu	Lys	Asn	Leu	Leu	Leu	Asn
					885						890					895	
		Arg	Lys	Thr	Leu	Gln	Thr	Val	Ala	Glu	Trp	Ile	Val	Asp	Asn	Trp	Tyr
					900					905					910		
40		Leu	Val	Val	Leu	Met	Gly	Val	Ala	Phe	Ile	Val	Val	Met	Gly	Ser	Phe
					915				920					925			
		Ile	Lys	Cys	Cys	Ala	Val	His	Thr	Pro	Ser	Ser	Asn	Pro	Lys	Lys	Arg
					930			935					940				
		Arg	Ala	Arg	Arg	Ile	Ser	Glu	Thr	Leu	Arg	Ala	Pro	Met	Asn	Thr	Leu
45		945					950					955					960
		Arg	Arg	Met	Gln	Arg	His	Pro	Asn	Gln	Arg	Gly	Ala	Gly	Pro	Arg	Ser
						965					970					975	
		Ile	Pro	Pro	Pro	Ala	His	Glu	Ala	Gln	His	Tyr	Ser	Arg	Gly	Gly	Asp
					980				985						990		
50		Gly	Arg	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Arg	His	Gly	Gly	Ser	Arg
					995				1000					1005			
		Ser	His	His	Gln	Gln	His	Pro	His	Asp	Trp	Asp	Arg	His	Gln	Gly	Gly
					1010			1015				1020					
55		His	Ser	Ile	Val	Pro	Leu	Pro	Thr	Gly	Gly	Ser	His	Ser	Ser	Arg	Asn
		1025					1030					1035					1040

	Ser	Ala	Ala	Asn	Gln	Ala	Arg	Arg	Ser	Asp	Gly	Arg	Gly	Pro	Arg	Ser	
					1045					1050					1055		
	Thr	Ser	Ser	Gly	Arg	Pro	Gln	Ala	Ile	Ala	Ser	Gly	Ser	Gly	Ala	Ala	
				1060					1065					1070			
5	Ser	Gly	Ala	Ala	Arg	Ser	His	Gly	Gly	Tyr	Gly	Ala	Glu	Gln	Ala	Ile	
			1075					1080					1085				
	Pro	Gly	Ser	Ile	Gly	Gly	Gly	Val	Gln	Ala	Ala	Ile	Ser	Ser	Gly	Gly	
			1090				1095					1100					
	Val	Val	Ala	Arg	Ala	Gln	Leu	Pro	Leu	Pro	Leu	Pro	Pro	Pro	Asn	Gly	
10			1105			1110				1115					1120		
	Gln	Gln	Gln	Met	Gln	Gln	Gln	Gln	Gln	Leu	Gln	Leu	Gln	Gln	Pro	Ala	
				1125					1130					1135			
	Ile	Ser	Pro	Gln	Gln	Gln	Pro	Gln	Gln	Ala	Phe	Tyr	Thr	Pro	Lys	Glu	
			1140					1145				1150					
15	Leu	Pro	Pro	Arg	Asn	Lys	Ser	Arg	Ser	Ser	Arg	Thr	Asn	Asn	Thr	Ser	
			1155					1160				1165					
	Asn	Thr	Thr	Thr	Thr	Thr	Asn	Ser	Ser	Thr	Ala	Ala	Ala	Gly	Ser	Gly	
			1170				1175				1180						
	Ser	Val	Ser	Gly	Pro	Gly	Ser	Gly	Ala	Gly	Ser	Ser	Ser	Lys	Ser	Lys	
20			1185			1190				1195				1200			
	Ser	Gly	Lys	Ser	Ala	Lys	Ala	Lys	Asp	Ser	Lys	Ser	Gln	Lys	Ser	Gln	
				1205					1210				1215				
	Gln	Ala	Asn	Asn	Ser	Arg	Ser	Ser	Ser	Lys	Glu	Lys	Gly	Val	Lys	Pro	
			1220					1225				1230					
25	Val	Arg	Arg	Asn	Ile	Val	Tyr										
			1235														

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2796 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

	GAATTC	CGGG	TTTT	GGAG	GACT	AGAG	CGCT	TTGC	CGGC	CCCT	CTGA	AGTG	GGA	GCG	AGAG	GGGA	60
	GGTG	CTTT	CG	CCGT	TCTC	CT	GCC	AGG	GGG	AG	GTCC	CGG	CTT	CCCG	TGG	AGG	120
	AGCC	CCTT	CA	GCTT	CTCC	CT	CCG	GAT	CGAT	GTG	CTG	CTGT	TAAC	CCG	TGA	GGAG	180
	GCGG	CGGC	CAG	CGGC	AG	CGG	AG	CGG	AG	CGG	AG	CGG	AG	CGG	AG	CGG	240
40	GGCG	GCGG	GGG	ATGG	GAGG	TC	AGT	ATG	GGG	AA	TCCT	TTAA	AT	AA	TAT	ATCA	300
	AGGA	TAT	CT	TACA	ATG	TGG	ATTC	ATT	AC	CA	AAAA	AC	CA	GC	GT	GCCA	360
	CTCA	CAT	GAA	GACCA	ATTTT	TAC	GT	CT	AGA	TTT	CC	CAT	GCC	CAT	GGA	AGAC	420
	ACGA	ATGA	AG	AGGG	ACACTT	CCCT	TTTT	CAG	TGAT	GAATTT	AAAG	TAG	AAA	CAT	CAA	ATAA	480
	AGTA	CTTG	AT	TATG	ATACCT	CTCA	TATTTA	CACT	GGAC	ATTTAT	GGTG	AAGA	AGGA	AG			540
45	TTTA	GCC	ATG	GGT	CTGTTAT	TGAT	GGA	AGA	TTTGA	AGGAT	TCAT	CCAG	AC	TCGT	GGT	GGC	600
	ACAT	TTTT	ATG	TTTG	AGCCAG	CAG	AGAG	ATA	TATTA	AGAC	CGAA	CTCT	GC	CATT	TTCA	CTC	660
	TGTC	ATTT	AT	CATGA	AGATG	ATATTA	ACTA	TCCC	CATA	AAA	TACG	GTCC	TC	AGGG	GGG	CTG	720
	TGC	AGAT	CAT	TCAG	TATTG	AAAG	AATG	AG	GAA	ATACC	AG	ATGA	CTGG	TG	TAG	AGGA	780
	AAC	ACAG	ATA	CCTCA	AGAAG	AAC	ATG	CTGC	TAAT	GGTCCA	GAAC	TTCT	GTA	GG	AAAA	ACG	840
50	TACA	AATT	CA	GCTG	AAAAAA	ATACT	TGTCA	GCTTT	TATAT	T	CAG	ACTG	ATC	ATT	TGT	TCTT	900
	TAA	ATATT	AC	GGA	ACACG	AG	AAGCT	GTG	AT	TGCC	CAG	ATA	TCC	AGT	CATG	TTAA	960
	TG	ATCA	AATT	TACC	AGACCA	CAG	ACTT	CTC	CGGA	ATCC	GT	AAC	ATC	AGT	T	TCAT	1020
	ACG	CATA	AGA	ATCA	ATA	CAA	CTG	CTG	ATGA	GAAGG	ACCCT	ACAA	ATC	CTT	TCCG	TTTCCC	1080
	AA	ATATT	GGT	GTGG	AGAAGT	TTCT	GGA	ATT	T	GAATT	CTG	AG	CA	ATC	ATG	ATGACT	1140
55	TTT	GGC	CTAT	GTCT	TACAG	ACCG	AGATT	T	TGAT	GAT	GGC	GTACT	TGG	T	TGGCT	TGGGT	1200

5 TGGAGCACCT TCAGGAAGCT CTGGAGGAAT ATGTGAAAAA AGTAAACTCT ATTCAGATGG 1260  
 TAAGAAGAAG TCCTTAAACA CTGGAATTAT TACTGTTCAG AACTATGGGT CTCATGTACC 1320  
 TCCCAAAGTC TCTCACATTA CTTTGTCTCA CGAAGTTGGA CATAACTTTG GATCCCCACA 1380  
 TGATTCTGGA ACAGAGTGCA CACCAGGAGA ATCTAAGAAT TTGGGTCAAA AAGAAAATGG 1440  
 CAATTACATC ATGTATGCAA GAGCAACATC TGGGGACAAA CTTAACAACA ATAAATTCTC 1500  
 ACTCTGTAGT ATTAGAAATA TAAGCCAAGT TCTTGAGAAG AAGAGAAACA ACTGTTTTGT 1560  
 TGAATCTGGC CAACCTATTT GTGGAAATGG AATGGTAGAA CAAGGTGAAG AATGTGATTG 1620  
 TGGCTATAGT GACCAGTGTA AAGATGAATG CTGCTTCGAT GCAAATCAAC CAGAGGGAAG 1680  
 AAAATGCAAA CTGAAACCTG GGAAACAGTG CAGTCCAAGT CAAGGTCCTT GTTGTACAGC 1740  
 10 ACAGTGTGCA TTCAAGTCAA AGTCTGAGAA GTGTCGGGAT GATTTCAGACT GTGCAAGGGA 1800  
 AGGAATATGT AATGGCTTCA CAGCTCTCTG CCCAGCATCT GACCCTAAAC CAAACTTCAC 1860  
 AGACTGTAAT AGGCATACAC AAGTGTGCAT TAATGGGCAA TGTGCAGGTT CTATCTGTGA 1920  
 GAAATATGGC TTAGAGGAGT GTACGTGTGC CAGTTCTGAT GGCAAAGATG ATAAAGAATT 1980  
 ATGCCATGTA TGCTGTATGA AGAAAATGGA CCCATCAACT TGTGCCAGTA CAGGGTCTGT 2040  
 15 GCAGTGGAGT AGGCACTTCA GTGGTCGAAC CATCACCTG CAACCTGGAT CCCCTTGCAA 2100  
 CGATTTTAGA GGTACTGTG ATGTTTTTCAT GCGGTGCAGA TTAGTAGATG CTGATGGTCC 2160  
 TCTAGCTAGG CTTAAAAAAG CAATTTTTCAT TCCAGAGCTC TATGAAAACA TTGCTGAATG 2220  
 GATTGTGGCT CATTGGTGGG CAGTATTACT TATGGGAATT GCTCTGATCA TGCTAATGGC 2280  
 TGGATTTATT AAGATATGCA GTGTTCATAC TCCAAGTAGT AATCCAAAGT TGCCTCCTCC 2340  
 20 TAAACCACTT CCAGGCACTT TAAAGAGGAG GAGACCTCCA CAGCCCATTC AGCAACCCCA 2400  
 GCGTCAGCGG CCCCAGAGAGA GTTATCAAAT GGGACACATG AGACGCTAAC TGCAGCTTTT 2460  
 GCCTTGTTTC TTCCTAGTGC CTACAATGGG AAAACTTCAC TCCAAAGAGA AACCTATTAA 2520  
 GTCATCATCT CCAAATAAA CCCTCACAAAG TAACAGTTGA AGAAAAATG GCAAGAGATC 2580  
 ATATCCTCAG ACCAGGTGGA ATTACTTAAA TTTTAAAGCC TGAAAATTCC AATTTGGGGG 2640  
 25 TGGGAGGTGG AAAAGGAACC CAATTTTCTT ATGAACAGAT ATTTTAACT TAATGGCACA 2700  
 AAGTCTTAGA ATATTATTAT GTGCCCCGTG TTCCCTGTTC TTCGTTGCTG CATTTTCTTC 2760  
 ACTTGCAGGC AACTTTGGCT CTCAATAAAC TTTTCG 2796

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Leu Leu Arg Val Leu Ile Leu Leu Leu Ser Trp Ala Ala Gly  
 1 5 10 15  
 Met Gly Gly Gln Tyr Gly Asn Pro Leu Asn Lys Tyr Ile Arg His Tyr  
 20 25 30  
 Glu Gly Leu Ser Tyr Asn Val Asp Ser Leu His Gln Lys His Gln Arg  
 35 40 45  
 Ala Lys Arg Ala Val Ser His Glu Asp Gln Phe Leu Arg Leu Asp Phe  
 50 55 60  
 His Ala His Gly Arg His Phe Asn Leu Arg Met Lys Arg Asp Thr Ser  
 65 70 75 80  
 Leu Phe Ser Asp Glu Phe Lys Val Glu Thr Ser Asn Lys Val Leu Asp  
 85 90 95  
 Tyr Asp Thr Ser His Ile Tyr Thr Gly His Ile Tyr Gly Glu Glu Gly  
 100 105 110  
 Ser Leu Ala Met Gly Leu Leu Leu Met Glu Asp Leu Lys Asp Ser Ser  
 115 120 125  
 Arg Leu Val Val Ala His Phe Met Phe Glu Pro Ala Glu Arg Tyr Ile  
 130 135 140  
 55 Lys Asp Arg Thr Leu Pro Phe His Ser Val Ile Tyr His Glu Asp Asp



	145		150		155		160									
	Ile	Asn	Tyr	Pro	His	Lys	Tyr	Gly	Pro	Gln	Gly	Gly	Cys	Ala	Asp	His
					165					170					175	
5	Ser	Val	Phe	Glu	Arg	Met	Arg	Lys	Tyr	Gln	Met	Thr	Gly	Val	Glu	Glu
				180					185					190		
	Val	Thr	Gln	Ile	Pro	Gln	Glu	Glu	His	Ala	Ala	Asn	Gly	Pro	Glu	Leu
			195					200					205			
	Leu	Arg	Lys	Lys	Arg	Thr	Asn	Ser	Ala	Glu	Lys	Asn	Thr	Cys	Gln	Leu
		210					215					220				
10	Tyr	Ile	Gln	Thr	Asp	His	Leu	Phe	Phe	Lys	Tyr	Tyr	Gly	Thr	Arg	Glu
	225					230					235					240
	Ala	Val	Ile	Ala	Gln	Ile	Ser	Ser	His	Val	Lys	Ala	Ile	Asp	Thr	Ile
					245					250					255	
	Tyr	Gln	Thr	Thr	Asp	Phe	Ser	Gly	Ile	Arg	Asn	Ile	Ser	Phe	Met	Val
15				260					265					270		
	Lys	Arg	Ile	Arg	Ile	Asn	Thr	Thr	Ala	Asp	Glu	Lys	Asp	Pro	Thr	Asn
			275					280					285			
	Pro	Phe	Arg	Phe	Pro	Asn	Ile	Gly	Val	Glu	Lys	Phe	Leu	Glu	Leu	Asn
		290					295					300				
20	Ser	Glu	Gln	Asn	His	Asp	Asp	Tyr	Cys	Leu	Ala	Tyr	Val	Phe	Thr	Asp
	305					310					315					320
	Arg	Asp	Phe	Asp	Asp	Gly	Val	Leu	Gly	Leu	Ala	Trp	Val	Gly	Ala	Pro
					325					330					335	
	Ser	Gly	Ser	Ser	Gly	Gly	Ile	Cys	Glu	Lys	Ser	Lys	Leu	Tyr	Ser	Asp
25				340					345					350		
	Gly	Lys	Lys	Lys	Ser	Leu	Asn	Thr	Gly	Ile	Ile	Thr	Val	Gln	Asn	Tyr
		355						360					365			
	Gly	Ser	His	Val	Pro	Pro	Lys	Val	Ser	His	Ile	Thr	Phe	Ala	His	Glu
		370					375					380				
30	Val	Gly	His	Asn	Phe	Gly	Ser	Pro	His	Asp	Ser	Gly	Thr	Glu	Cys	Thr
	385					390					395					400
	Pro	Gly	Glu	Ser	Lys	Asn	Leu	Gly	Gln	Lys	Glu	Asn	Gly	Asn	Tyr	Ile
				405						410					415	
	Met	Tyr	Ala	Arg	Ala	Thr	Ser	Gly	Asp	Lys	Leu	Asn	Asn	Asn	Lys	Phe
35				420					425					430		
	Ser	Leu	Cys	Ser	Ile	Arg	Asn	Ile	Ser	Gln	Val	Leu	Glu	Lys	Lys	Arg
		435						440					445			
	Asn	Asn	Cys	Phe	Val	Glu	Ser	Gly	Gln	Pro	Ile	Cys	Gly	Asn	Gly	Met
		450					455					460				
40	Val	Glu	Gln	Gly	Glu	Glu	Cys	Asp	Cys	Gly	Tyr	Ser	Asp	Gln	Cys	Lys
	465					470					475					480
	Asp	Glu	Cys	Cys	Phe	Asp	Ala	Asn	Gln	Pro	Glu	Gly	Arg	Lys	Cys	Lys
					485					490					495	
	Leu	Lys	Pro	Gly	Lys	Gln	Cys	Ser	Pro	Ser	Gln	Gly	Pro	Cys	Cys	Thr
45				500					505					510		
	Ala	Gln	Cys	Ala	Phe	Lys	Ser	Lys	Ser	Glu	Lys	Cys	Arg	Asp	Asp	Ser
		515						520					525			
	Asp	Cys	Ala	Arg	Glu	Gly	Ile	Cys	Asn	Gly	Phe	Thr	Ala	Leu	Cys	Pro
		530					535					540				
50	Ala	Ser	Asp	Pro	Lys	Pro	Asn	Phe	Thr	Asp	Cys	Asn	Arg	His	Thr	Gln
	545					550					555					560
	Val	Cys	Ile	Asn	Gly	Gln	Cys	Ala	Gly	Ser	Ile	Cys	Glu	Lys	Tyr	Gly
				565						570					575	
	Leu	Glu	Glu	Cys	Thr	Cys	Ala	Ser	Ser	Asp	Gly	Lys	Asp	Asp	Lys	Glu
55				580					585					590		



Leu Cys His Val Cys Cys Met Lys Lys Met Asp Pro Ser Thr Cys Ala  
 595 600 605  
 Ser Thr Gly Ser Val Gln Trp Ser Arg His Phe Ser Gly Arg Thr Ile  
 610 615 620  
 Thr Leu Gln Pro Gly Ser Pro Cys Asn Asp Phe Arg Gly Tyr Cys Asp  
 625 630 635 640  
 Val Phe Met Arg Cys Arg Leu Val Asp Ala Asp Gly Pro Leu Ala Arg  
 645 650 655  
 Leu Lys Lys Ala Ile Phe Ser Pro Glu Leu Tyr Glu Asn Ile Ala Glu  
 660 665 670  
 Trp Ile Val Ala His Trp Trp Ala Val Leu Leu Met Gly Ile Ala Leu  
 675 680 685  
 Ile Met Leu Met Ala Gly Phe Ile Lys Ile Cys Ser Val His Thr Pro  
 690 695 700  
 Ser Ser Asn Pro Lys Leu Pro Pro Pro Lys Pro Leu Pro Gly Thr Leu  
 705 710 715 720  
 Lys Arg Arg Arg Pro Pro Gln Pro Ile Gln Gln Pro Gln Arg Gln Arg  
 725 730 735  
 Pro Arg Glu Ser Tyr Gln Met Gly His Met Arg Arg  
 740 745

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2098 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCTGAG	CAGAATCATG	ATGACTACTG	TTTGGCCTAT	GTCTTCACAG	ACCGAGATTT	60
TGATGATGGC	GTACTTGGTC	TGGCTTGGGT	TGGAGCACCT	TCAGGAAGCT	CTGGAGGAAT	120
ATGTGAAAAA	AGTAACTCT	ATTCAGATGG	TAAGAAGAAG	TCCTTAAACA	CTGGAATTAT	180
TACTGTTTCA	AACTATGGGT	CTCATGTACC	TCCCAAAGTC	TCTCACATTA	CTTTTGCTCA	240
CGAAGTTGGA	CATAACTTTG	GATCCCCACA	TGATTCTGGA	ACAGAGTGCA	CACCAGGAGA	300
ATCTAAGAAT	TTGGGTCAAA	AAGAAAATGG	CAATTACATC	ATGTATGCAA	GAGCAACATC	360
TGGGGACAAA	CTTAACAACA	ATAAATTCTC	ACTCTGTAGT	ATTAGAAATA	TAAGCCAAGT	420
TCTTGAGAAG	AAGAGAAACA	ACTGTTTTGT	TGAATCTGGC	CAACCTATTT	GTGGAAATGG	480
AATGGTAGAA	CAAGGTGAAG	AATGTGATTG	TGGCTATAGT	GACCAGTGTA	AAGATGAATG	540
CTGCTTCGAT	GCAAATCAAC	CAGAGGGAAG	AAAATGCAAA	CTGAAACCTG	GGAAACAGTG	600
CAGTCCAAGT	CAAGGTCCTT	GTTGTACAGC	ACAGTGTGCA	TTCAAGTCAA	AGTCTGAGAA	660
GTGTCGGGAT	GATTCAGACT	GTGCAAGGGA	AGGAATATGT	AATGGCTTCA	CAGCTCTCTG	720
CCCAGCATCT	GACCCTAAAC	CAAACCTCAC	AGACTGTAAT	AGGCATACAC	AAGTGTGCAT	780
TAATGGGGTA	AGCATTTAAC	TATATGTTTT	AAAATTTAAT	TTTAGAAAAC	TTGTTTTTCA	840
GAAGAATTAT	TGATGCTTAA	AGCTACATAG	TTAAAGTAAT	TAATCTTGGT	CTCTGTTTAA	900
GTAATATTCC	CTCACAACAA	CATGAATATA	TTATGTGGCA	TTCAATTAGC	TACTAATTTG	960
TCTTTCATCT	TTCCATGTAC	ATGTGGTTGA	TATTCTCTAG	AGAAACATAG	TTGTACAACT	1020
CGGCATGTGA	TTTGTCTATA	ATATTTAAGT	TTTATAAAAT	AATATTTTCA	TAGCCTAAAT	1080
AAAAGAAGTC	TTTGGTTCATC	TTCTCTGAAT	ATCAAACCTT	CAAAGCTTTT	GTGGCTGAAT	1140
ATCACTTTGC	TCTACAGGAA	AAAAATTTAA	TTTTTCTTTC	TTTATAGAAG	AGCCGTAATA	1200
ACCAACATAA	AATCGATCCT	CATCTAATCT	CTTGCTCTGC	TTTTATTTC	TTTTTTTAAAG	1260
TTGCCATTGC	TTTAAAAGAT	TTACTATCTT	TCTTGGATTT	ACTGTTTTTC	AAATTTTTTTC	1320
AAATGTATTT	ATGTAATTCA	GTTTTGATAC	TCATCTCTGT	TTGTTTTTCA	CTTTCATTTT	1380
CATTTAAATA	TTTTGACATT	GGAAGCTCAT	ACTTGCCTGT	CTGTTACTAT	AAAAAATAGG	1440
TTTGACTGTA	TAGGGATTAA	ACAATTTGTC	TTTTATTTTC	TTCTAGCAAT	GTGCAGGTTC	1500
TATCTGTGAG	AAATATGGCT	TAGAAGAGTG	TACGTGTGCC	AGTCTGATGG	CAAAGATGAT	1560

AAAGAATTAT GCCATGTATG CTGTATGAAG AAAAGTAAGG CTTTAAATAA CACAAGATAT 1620  
 AAAATTTGCC TCAAACTATT ATTTTCTCCT AAATTTTAAG TGAAAACTT TGACCTACAG 1680  
 TTTGGCCAGA TAATTTCCAG CTAAATCTGT CCTCTTGAGG AGATTATAAA TGTAACGTAG 1740  
 CATTGTGTCT CTATTATTAT GGTCTCTACA ATGTTTTTAA AATGATAAAC TAGACAAAAC 1800  
 GTTGCCAGCT TTACAGCAGT AATTTACATA AACACTGTTA GACTTTAAGT CATCGTGGAC 1860  
 ACTGAGTCAA GACTTGCTGG TTGCTTGTTT ACATTGTAAC ATTTAATATG AATTACTGAT 1920  
 GCGGTTACCC AGCCTAACTA GAGAAGGTCT GTATAACATG TTATGGTAAT GATTTTCAGTT 1980  
 TTTTTTCCCT CTTTGTATTT GCACAACCTGG GAAATCTGAT CTGCAACTTA TATTTGAATC 2040  
 TGACCTTCAG CTTATATTTG GCATTTCTTT TCCAGTGGAC CCATCAACTC CGGAATTC 2098

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 265 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asn	Ser	Glu	Gln	Asn	His	Asp	Asp	Tyr	Cys	Leu	Ala	Tyr	Val	Phe	Thr
1				5					10					15	
Asp	Arg	Asp	Phe	Asp	Asp	Gly	Val	Leu	Gly	Leu	Ala	Trp	Val	Gly	Ala
			20					25					30		
Pro	Ser	Gly	Ser	Ser	Gly	Gly	Ile	Cys	Glu	Lys	Ser	Lys	Leu	Tyr	Ser
		35				40					45				
Asp	Gly	Lys	Lys	Lys	Ser	Leu	Asn	Thr	Gly	Ile	Ile	Thr	Val	Gln	Asn
	50					55					60				
Tyr	Gly	Ser	His	Val	Pro	Pro	Lys	Val	Ser	His	Ile	Thr	Phe	Ala	His
65					70					75					80
Glu	Val	Gly	His	Asn	Phe	Gly	Ser	Pro	His	Asp	Ser	Gly	Thr	Glu	Cys
				85				90					95		
Thr	Pro	Gly	Glu	Ser	Lys	Asn	Leu	Gly	Gln	Lys	Glu	Asn	Gly	Asn	Tyr
			100					105					110		
Ile	Met	Tyr	Ala	Arg	Ala	Thr	Ser	Gly	Asp	Lys	Leu	Asn	Asn	Asn	Lys
		115					120					125			
Phe	Ser	Leu	Cys	Ser	Ile	Arg	Asn	Ile	Ser	Gln	Val	Leu	Glu	Lys	Lys
	130					135					140				
Arg	Asn	Asn	Cys	Phe	Val	Glu	Ser	Gly	Gln	Pro	Ile	Cys	Gly	Asn	Gly
145					150					155					160
Met	Val	Glu	Gln	Gly	Glu	Glu	Cys	Asp	Cys	Gly	Tyr	Ser	Asp	Gln	Cys
			165					170						175	
Lys	Asp	Glu	Cys	Cys	Phe	Asp	Ala	Asn	Gln	Pro	Glu	Gly	Arg	Lys	Cys
			180					185					190		
Lys	Leu	Lys	Pro	Gly	Lys	Gln	Cys	Ser	Pro	Ser	Gln	Gly	Pro	Cys	Cys
		195					200					205			
Thr	Ala	Gln	Cys	Ala	Phe	Lys	Ser	Lys	Ser	Glu	Lys	Cys	Arg	Asp	Asp
	210					215						220			
Ser	Asp	Cys	Ala	Arg	Glu	Gly	Ile	Cys	Asn	Gly	Phe	Thr	Ala	Leu	Cys
225					230					235					240
Pro	Ala	Ser	Asp	Pro	Lys	Pro	Asn	Phe	Thr	Asp	Cys	Asn	Arg	His	Thr
			245						250					255	
Gln	Val	Cys	Ile	Asn	Gly	Val	Ser	Ile							
			260					265							

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2481 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

5	CCGTGAGGAG	GCGGCGGCCG	GGAAGATGGT	GTTGCCGACA	GTGTTAATTC	TGCTCCTCTC	60
	CTGGGCGGCG	GGGCTGGGAG	GTCAGTATGG	AAATCCTTTA	AATAAATATA	TTAGACATTA	120
	TGAAGGATTA	TCTTACAATG	TGGATTTCAT	ACACCAAAAA	CACCAGCGTG	CCAAACGAGC	180
10	AGTCTCACAT	GAGGACCAGT	TTTTACTTCT	AGATTTCCAT	GCTCATGGAA	GACAGTTCAA	240
	CCTACGAATG	AAGAGGGACA	CTTCCCTTTT	TAGTGATGAA	TTTAAAGTAG	AAACATCAAA	300
	TAAAGTACTT	GATTATGATA	CCTCTCATAT	TTACACTGGA	CATATTTATG	GTGAAGAAGG	360
	AAGCTTTAGT	CATGGGTCTG	TCATTGATGG	AAGATTTGAA	GGTTTCATCA	AGACTCGTGG	420
	TGGCACGTTT	TACATTGAGC	CAGCAGAGAG	ATACATTAAA	GATCGAATCC	TGCCATTTCA	480
15	CTCTGTCATT	TATCATGAAG	ATGATATTAA	CTATCCCCAT	AAATACGGCC	CACAGGGGGG	540
	CTGTGCAGAT	CACTCCGTTT	TTGAAAGGAT	GAGGAAGTAC	CAAATGACTG	GAGTAGAGGA	600
	AGGAGCCCGG	GCACATCCAG	AGAAGCATGC	TGCTAGTAGT	GGTCCTGAGC	TCCTGAGGAA	660
	AAAACGCACA	ACTCTGGCTG	AAAGAAATAC	TTGTCAGCTC	TATATCCAGA	CAGATCACCT	720
	GTTCTTTAAA	TACTATGGAA	CACGAGAAGC	TGTGATTGCT	CAGATATCCA	GTCATGTTAA	780
20	AGCAATTGAT	ACAATTTACC	AGACTACAGA	CTTCTCCGGA	ATCCGTAACA	TCAGCTTCAT	840
	GGTGAAACGC	ATAAGAATCA	ATACAACCTC	TGATGAAAAA	GACCCTACAA	ATCCTTTCCG	900
	TTTCCCAAAT	ATTGGTGTGG	AGAAGTTCCT	GGAGTTGAAT	TCTGAGCAGA	ATCATGATGA	960
	CTACTGCCTG	GCCTATGTCT	TCACAGACCG	GGATTTTGAT	GATGGTGTTT	TTGGTCTGGC	1020
	CTGGGTTGGA	GCACCTTCAG	GAAGCTCTGG	GGGAATATGT	GAGAAAAGCA	AGTTGTATTC	1080
25	AGATGGCAAG	AAGAAGTCAT	TGAACACAGG	CATCATTACT	GTTTCAGAAT	ATGGCTCCCA	1140
	TGTGCCTCCC	AAAGTCTCTC	ATATTACGTT	TGCTCATGAA	GTTGGACATA	ACTTTGGATC	1200
	TCCACATGAT	TCTGGAACAG	AGTGTACTCC	AGGAGAGTCT	AAGAACTTAG	GACAAAAAGA	1260
	AAATGGCAAT	TACATCATGT	ATGCAAGAGC	AACATCTGGG	GACAACTTA	ACAACAACAA	1320
	ATTTTCACTC	TGCAGCATT	GAAACATAAG	CCAAGTGCTT	GAGAAGAAGA	GGAACAACCTG	1380
30	TTTTGTGAA	TCTGGCCAGC	CTATCTGTGG	AAACGGGATG	GTGGAACAAG	GGGAAGAGTG	1440
	TGACTGTGGC	TACAGTGACC	AGTGCAAAGA	TGATTGCTGC	TTGATGCCA	ACCAGCCAGA	1500
	GGGGAAGAAA	TGCAAGCTGA	AGCCTGGGAA	GCAGTGCAGT	CCGAGTCAAG	GACCTGTCTG	1560
	TACAGCACAG	TGTGCATTCA	AGTCAAAGTC	TGAAAAGTGC	CGGGATGATT	CTGACTGTGC	1620
	AAAGGAAGGG	ATATGCAATG	GCTTCACAGC	CCTTTGCCCA	GCATCTGATC	CCAAGCCCAA	1680
35	CTTTACAGAC	TGTAACAGGC	ACACACAAGT	GTGCATTAAT	GGGCAATGTG	CAGGTTCTAT	1740
	TTGTGAAAAG	TATGACTTGG	AGGAGTGCAC	CTGTGCCAGC	TCTGATGGCA	AAGATAATAA	1800
	GGAATTATGC	CATGTTTGCT	GCATGAAGAA	AATGGCTCCA	TCAACTTGTG	CCAGTACAGG	1860
	CTCTTTGCAG	TGGAGCAAGC	AGTTCAGTGG	TCGGACTATC	ACTCTGCAGC	CGGGCTCTCC	1920
	ATGTAATGAC	TTCAGAGGCT	ACTGTGATGT	TTTCATGCGG	TGCAGATTAG	TAGATGCTGA	1980
40	TGGCCCTCTA	GCTAGGCTGA	AAAAAGCCAT	TTTTAGTCCA	CAACTCTATG	AAAACATTGC	2040
	TGAGTGGATT	GTGGCTCACT	GGTGGGCAGT	ACTGCTTATG	GGAATTGCCC	TGATCATGTT	2100
	AATGGCTGGA	TTTATCAAGA	TTTGCAGTGT	TCACACTCCA	AGTAGTAATC	CAAAGTTGCC	2160
	GCCTCCTAAA	CCACTTCCAG	GCACTTTAAA	GAGGAGGAGA	CCGCCACAGC	CCATTCAGCA	2220
	GCCCCGCGT	CAGAGGCCCC	GAGAGAGTTA	TCAAATGGGA	CACATGCGAC	GCTAATGCAG	2280
45	CTTTTGCCTT	GGTTCTTCCT	AGTGCCTACA	GTGGGAAAAC	TTCACTCCAA	AGAGAAACCT	2340
	GTTAAGTCAT	CATCTGCAAA	TGATACCCTT	ACAGTTAATA	GTTGAAGAAA	AAATGGCAAG	2400
	AGATCATGTC	CTCAGATCAG	GTGGAATTAC	TCAAATTTA	AAGCCTGAAA	ATTCCAATTT	2460
	TGGGGGTGGG	GGTGGGATGG	G				2481

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 749 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Val	Leu	Pro	Thr	Val	Leu	Ile	Leu	Leu	Leu	Ser	Trp	Ala	Ala	Gly
1				5				10						15	
Leu	Gly	Gly	Gln	Tyr	Gly	Asn	Pro	Leu	Asn	Lys	Tyr	Ile	Arg	His	Tyr
			20					25					30		
Glu	Gly	Leu	Ser	Tyr	Asn	Val	Asp	Ser	Leu	His	Gln	Lys	His	Gln	Arg
		35					40					45			
Ala	Lys	Arg	Ala	Val	Ser	His	Glu	Asp	Gln	Phe	Leu	Leu	Leu	Asp	Phe
	50					55					60				
His	Ala	His	Gly	Arg	Gln	Phe	Asn	Leu	Arg	Met	Lys	Arg	Asp	Thr	Ser
65					70					75				80	
Leu	Phe	Ser	Asp	Glu	Phe	Lys	Val	Glu	Thr	Ser	Asn	Lys	Val	Leu	Asp
			85						90					95	
Tyr	Asp	Thr	Ser	His	Ile	Tyr	Thr	Gly	His	Ile	Tyr	Gly	Glu	Glu	Gly
			100					105					110		
Ser	Phe	Ser	His	Gly	Ser	Val	Ile	Asp	Gly	Arg	Phe	Glu	Gly	Phe	Ile
		115					120					125			
Lys	Thr	Arg	Gly	Gly	Thr	Phe	Tyr	Ile	Glu	Pro	Ala	Glu	Arg	Tyr	Ile
	130					135					140				
Lys	Asp	Arg	Ile	Leu	Pro	Phe	His	Ser	Val	Ile	Tyr	His	Glu	Asp	Asp
145					150					155				160	
Ile	Asn	Tyr	Pro	His	Lys	Tyr	Gly	Pro	Gln	Gly	Gly	Cys	Ala	Asp	His
			165						170					175	
Ser	Val	Phe	Glu	Arg	Met	Arg	Lys	Tyr	Gln	Met	Thr	Gly	Val	Glu	Glu
			180					185					190		
Gly	Ala	Arg	Ala	His	Pro	Glu	Lys	His	Ala	Ala	Ser	Ser	Gly	Pro	Glu
	195					200						205			
Leu	Leu	Arg	Lys	Lys	Arg	Thr	Thr	Leu	Ala	Glu	Arg	Asn	Thr	Cys	Gln
	210					215						220			
Leu	Tyr	Ile	Gln	Thr	Asp	His	Leu	Phe	Phe	Lys	Tyr	Tyr	Gly	Thr	Arg
225					230					235				240	
Glu	Ala	Val	Ile	Ala	Gln	Ile	Ser	Ser	His	Val	Lys	Ala	Ile	Asp	Thr
			245						250					255	
Ile	Tyr	Gln	Thr	Thr	Asp	Phe	Ser	Gly	Ile	Arg	Asn	Ile	Ser	Phe	Met
		260						265					270		
Val	Lys	Arg	Ile	Arg	Ile	Asn	Thr	Thr	Ser	Asp	Glu	Lys	Asp	Pro	Thr
		275					280						285		
Asn	Pro	Phe	Arg	Phe	Pro	Asn	Ile	Gly	Val	Glu	Lys	Phe	Leu	Glu	Leu
	290					295						300			
Asn	Ser	Glu	Gln	Asn	His	Asp	Asp	Tyr	Cys	Leu	Ala	Tyr	Val	Phe	Thr
305					310					315				320	
Asp	Arg	Asp	Phe	Asp	Asp	Gly	Val	Leu	Gly	Leu	Ala	Trp	Val	Gly	Ala
			325						330					335	
Pro	Ser	Gly	Ser	Ser	Gly	Gly	Ile	Cys	Glu	Lys	Ser	Lys	Leu	Tyr	Ser
		340					345						350		
Asp	Gly	Lys	Lys	Lys	Ser	Leu	Asn	Thr	Gly	Ile	Ile	Thr	Val	Gln	Asn
		355					360					365			
Tyr	Gly	Ser	His	Val	Pro	Pro	Lys	Val	Ser	His	Ile	Thr	Phe	Ala	His
	370					375					380				
Glu	Val	Gly	His	Asn	Phe	Gly	Ser	Pro	His	Asp	Ser	Gly	Thr	Glu	Cys
385					390					395				400	
Thr	Pro	Gly	Glu	Ser	Lys	Asn	Leu	Gly	Gln	Lys	Glu	Asn	Gly	Asn	Tyr
			405						410					415	
Ile	Met	Tyr	Ala	Arg	Ala	Thr	Ser	Gly	Asp	Lys	Leu	Asn	Asn	Asn	Lys

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			420					425					430				
Phe	Ser	Leu	Cys	Ser	Ile	Arg	Asn	Ile	Ser	Gln	Val	Leu	Glu	Lys	Lys		
			435					440					445				
Arg	Asn	Asn	Cys	Phe	Val	Glu	Ser	Gly	Gln	Pro	Ile	Cys	Gly	Asn	Gly		
			450					455					460				
Met	Val	Glu	Gln	Gly	Glu	Glu	Cys	Asp	Cys	Gly	Tyr	Ser	Asp	Gln	Cys		
465						470					475				480		
Lys	Asp	Asp	Cys	Cys	Phe	Asp	Ala	Asn	Gln	Pro	Glu	Gly	Lys	Lys	Cys		
				485					490						495		
Lys	Leu	Lys	Pro	Gly	Lys	Gln	Cys	Ser	Pro	Ser	Gln	Gly	Pro	Cys	Cys		
			500					505					510				
Thr	Ala	Gln	Cys	Ala	Phe	Lys	Ser	Lys	Ser	Glu	Lys	Cys	Arg	Asp	Asp		
			515					520					525				
Ser	Asp	Cys	Ala	Lys	Glu	Gly	Ile	Cys	Asn	Gly	Phe	Thr	Ala	Leu	Cys		
			530					535				540					
Pro	Ala	Ser	Asp	Pro	Lys	Pro	Asn	Phe	Thr	Asp	Cys	Asn	Arg	His	Thr		
545						550				555					560		
Gln	Val	Cys	Ile	Asn	Gly	Gln	Cys	Ala	Gly	Ser	Ile	Cys	Glu	Lys	Tyr		
				565					570						575		
Asp	Leu	Glu	Glu	Cys	Thr	Cys	Ala	Ser	Ser	Asp	Gly	Lys	Asp	Asn	Lys		
			580					585					590				
Glu	Leu	Cys	His	Val	Cys	Cys	Met	Lys	Lys	Met	Ala	Pro	Ser	Thr	Cys		
			595				600					605					
Ala	Ser	Thr	Gly	Ser	Leu	Gln	Trp	Ser	Lys	Gln	Phe	Ser	Gly	Arg	Thr		
			610				615					620					
Ile	Thr	Leu	Gln	Pro	Gly	Ser	Pro	Cys	Asn	Asp	Phe	Arg	Gly	Tyr	Cys		
625					630					635					640		
Asp	Val	Phe	Met	Arg	Cys	Arg	Leu	Val	Asp	Ala	Asp	Gly	Pro	Leu	Ala		
				645					650						655		
Arg	Leu	Lys	Lys	Ala	Ile	Phe	Ser	Pro	Gln	Leu	Tyr	Glu	Asn	Ile	Ala		
			660					665					670				
Glu	Trp	Ile	Val	Ala	His	Trp	Trp	Ala	Val	Leu	Leu	Met	Gly	Ile	Ala		
			675				680					685					
Leu	Ile	Met	Leu	Met	Ala	Gly	Phe	Ile	Lys	Ile	Cys	Ser	Val	His	Thr		
			690				695					700					
Pro	Ser	Ser	Asn	Pro	Lys	Leu	Pro	Pro	Pro	Lys	Pro	Leu	Pro	Gly	Thr		
705					710					715					720		
Leu	Lys	Arg	Arg	Arg	Pro	Pro	Gln	Pro	Ile	Gln	Gln	Pro	Pro	Arg	Gln		
				725					730						735		
Arg	Pro	Arg	Glu	Ser	Tyr	Gln	Met	Gly	His	Met	Arg	Arg					
			740					745									